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Sequence Listing was accepted.

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Reviewer: Durreshwar Anjum

Timestamp: [year=2009; month=9; day=23; hr=14; min=11; sec=26; ms=440; ]

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Application No: 10554387

Version No: 3.0

Input Set:

Output Set:

Started: 2009-09-22 13:22:09.739

Finished: 2009-09-22 13:22:11.086

Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 347 ms

Total Warnings: 11

Total Errors: 0

No. of SeqIDs Defined: 14

Actual SeqID Count: 14

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (2)
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W 213	Artificial or Unknown found in <213> in SEQ ID (4)
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W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)

SEQUENCE LISTING

<110> Protalix Ltd.  
Shaaltiel, Yoseph  
Baum, Gideon  
Hashmueli, Sharon  
Lewkowitz, Ayala  
Bartfeld, Daniel

<120> PRODUCTION OF HIGH MANNOSE PROTEINS IN PLANT CULTURE

<130> 30570

<140> 10554387

<141> 2005-10-25

<150> IL 155588

<151> 2003-04-27

<150> PCT/IL2004/000181

<151> 2004-02-24

<160> 14

<170> PatentIn version 3.5

<210> 1

<211> 22

<212> PRT

<213> Artificial sequence

<220>

<223> ER signal peptide

<400> 1

Met Lys Thr Asn Leu Phe Leu Phe Leu Ile Phe Ser Leu Leu Leu Ser  
1 5 10 15

Leu Ser Ser Ala Glu Phe  
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<210> 2

<211> 7

<212> PRT

<213> Artificial sequence

<220>

<223> Vacuolar targeting signal from Tobacco chitinase A

<400> 2

Asp Leu Leu Val Asp Thr Met  
1 5

<210> 3  
 <211> 21  
 <212> DNA  
 <213> Artificial sequence  
  
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 <223> Single strand DNA oligonucleotide  
  
 <400> 3  
 cagaattcgc cgcgccctgc a 21

<210> 4  
 <211> 22  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> Single strand DNA oligonucleotide  
  
 <400> 4  
 ctcagatctt ggcgatgcca ca 22

<210> 5  
 <211> 19  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> Single strand DNA oligonucleotide  
  
 <400> 5  
 ctcagaagac cagagggct 19

<210> 6  
 <211> 17  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> Single strand DNA oligonucleotide  
  
 <400> 6  
 caaagcggcc atcgtgc 17

<210> 7  
 <211> 1491  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 7  
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acatactgtg actcctttga cccccgacc tttcctgccc ttggtacctt cagecgctat 120  
 gagagtacac gcagtgggcg acggatggag ctgagtatgg ggcccatcca ggctaatacac 180  
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 gatttccagt tgcacaactt cagcctccca gaggaagata ccaagctcaa gataccctg 480  
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<210> 8

<211> 497

<212> PRT

<213> Homo sapiens

<400> 8

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 Ala Leu Gly Thr Phe Ser Arg Tyr Glu Ser Thr Arg Ser Gly Arg Arg  
                           35                    40                    45  
 Met Glu Leu Ser Met Gly Pro Ile Gln Ala Asn His Thr Gly Thr Gly  
                           50                    55                    60  
 Leu Leu Leu Thr Leu Gln Pro Glu Gln Lys Phe Gln Lys Val Lys Gly  
                           65                    70                    75                    80  
 Phe Gly Gly Ala Met Thr Asp Ala Ala Ala Leu Asn Ile Leu Ala Leu  
                           85                    90                    95  
 Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys Ser Tyr Phe Ser Glu Glu  
                           100                    105                    110  
 Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro Met Ala Ser Cys Asp Phe  
                           115                    120                    125  
 Ser Ile Arg Thr Tyr Thr Tyr Ala Asp Thr Pro Asp Asp Phe Gln Leu  
                           130                    135                    140  
 His Asn Phe Ser Leu Pro Glu Glu Asp Thr Lys Leu Lys Ile Pro Leu  
                           145                    150                    155                    160  
 Ile His Arg Ala Leu Gln Leu Ala Gln Arg Pro Val Ser Leu Leu Ala  
                           165                    170                    175  
 Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys Thr Asn Gly Ala Val Asn  
                           180                    185                    190  
 Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly Asp Ile Tyr His Gln Thr  
                           195                    200                    205  
 Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp Ala Tyr Ala Glu His Lys  
                           210                    215                    220  
 Leu Gln Phe Trp Ala Val Thr Ala Glu Asn Glu Pro Ser Ala Gly Leu  
                           225                    230                    235                    240

Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly Phe Thr Pro Glu His Gln  
245 250 255

Arg Asp Phe Ile Ala Arg Asp Leu Gly Pro Thr Leu Ala Asn Ser Thr  
260 265 270

His His Asn Val Arg Leu Leu Met Leu Asp Asp Gln Arg Leu Leu Leu  
275 280 285

Pro His Trp Ala Lys Val Val Leu Thr Asp Pro Glu Ala Ala Lys Tyr  
290 295 300

Val His Gly Ile Ala Val His Trp Tyr Leu Asp Phe Leu Ala Pro Ala  
305 310 315 320

Lys Ala Thr Leu Gly Glu Thr His Arg Leu Phe Pro Asn Thr Met Leu  
325 330 335

Phe Ala Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser Val  
340 345 350

Arg Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile  
355 360 365

Thr Asn Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala  
370 375 380

Leu Asn Pro Glu Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser  
385 390 395 400

Pro Ile Ile Val Asp Ile Thr Lys Asp Thr Phe Tyr Lys Gln Pro Met  
405 410 415

Phe Tyr His Leu Gly His Phe Ser Lys Phe Ile Pro Glu Gly Ser Gln  
420 425 430

Arg Val Gly Leu Val Ala Ser Gln Lys Asn Asp Leu Asp Ala Val Ala  
435 440 445

Leu Met His Pro Asp Gly Ser Ala Val Val Val Val Leu Asn Arg Ser  
450 455 460

Ser Lys Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val Gly Phe Leu  
465 470 475 480

Glu Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp His Arg  
485 490 495

Gln

<210> 9  
<211> 338  
<212> DNA  
<213> Cauliflower mosaic virus

<400> 9  
ttttcacaaa gggtaatatc gggaaacctc ctcggattcc attgcccagc tatctgtcac 60  
ttcatcgaaa ggacagtaga aaaggaaggt ggctcctaca aatgcatca ttgcgataaa 120  
ggaaaggcta tcgttcaaga tgctctacc gacagtggtc ccaaagatgg acccccaccc 180  
acgaggaaca tcgtggaaaa agaagacggt ccaaccacgt cttcaaagca agtggattga 240  
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tcctctatat aaggaagttc atttcatttg gagaggac 338

<210> 10  
<211> 66  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Nucleic acid sequence encoding the ER signal peptide

<400> 10  
atgaagacta atctttttct ctttctcatc ttttcacttc tctatcatt atcctcggcc 60  
gaattc 66

<210> 11  
<211> 21  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Nucleic acid sequence encoding the vacuolar targeting sequence

<400> 11  
gatcttttag tcgatactat g 21



<210> 12  
<211> 167  
<212> DNA  
<213> Artificial sequence  
  
<220>  
<223> Nucleic acid sequence of the Agrobacterium tumefaciens terminator

<220>  
<221> misc\_feature  
<222> (162)..(162)  
<223> n is a, c, g, or t

<400> 12  
taatttcatg atctgttttg ttgtattccc ttgcaatgca gggcctaggg ctatgaataa 60  
agttaatgtg tgaatgtgtg aatgtgtgat tgtgacctga agggatcacg actataatcg 120  
tttataataa acaaagactt tgtcccaaaa accccccccc cngcaga 167

<210> 13  
<211> 2186  
<212> DNA  
<213> Artificial sequence

<220>  
<223> nucleic acid sequence encoding high mannose human  
glucocerebrosidase (GCD)

<220>  
<221> misc\_feature  
<222> (2181)..(2181)  
<223> n is a, c, g, or t

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ggaaaggcta tcgttcaaga tgcctctacc gacagtggtc ccaaagatgg acccccaccc 180  
acgaggaaca tcgtggaaaa agaagacggt ccaaccacgt cttcaaagca agtggattga 240  
tgtgatatct ccaactgacgt aagggatgac gcacaatccc actatccttc gcaagaccct 300  
tcctctatat aaggaagttc atttcatttg gagaggacag gcttcttgag atccttcaac 360  
aattaccaac aacaacaaac aacaacaaac attacaatta ctatttacia ttacagtcga 420  
gggatccaag gagatataac aatgaagact aatctttttc tcttttctcat cttttcactt 480  
ctcctatcat tctctcggc cgaattcgcc cgcccctgca tcctaaaag cttcggctac 540

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tgtattccct tgcaatgcag ggcttagggc tatgaataaa gttaatgtgt gaatgtgtga	2100
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gtccccaaaa ccccccccc ngcaga	2186

<210> 14

<211> 526

<212> PRT

<213> Artificial sequence

<220>

<223> High mannose human glucocerebrosidase (GCD)

<400> 14

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20 25 30

Tyr Ser Ser Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser Phe  
35 40 45

Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr Phe Ser Arg Tyr Glu Ser  
50 55 60

Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln Ala  
65 70 75 80

Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln Lys  
85 90 95

Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala Ala  
100 105 110

Leu Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys  
115 120 125

Ser Tyr Phe Ser Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro  
130 135 140

Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp Thr  
145 150 155 160

Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp Thr  
165 170 175

Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln Arg  
180 185 190

Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys  
195 200 205

Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly  
210 215 220

Asp Ile Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp  
225 230 235 240

Ala Tyr Ala Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu Asn  
245 250 255

Glu Pro Ser Ala Gly Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly  
260 265 270

Phe Thr Pro Glu His Gln Arg Asp Phe Ile Ala Arg Asp Leu Gly Pro  
275 280 285

Thr Leu Ala Asn Ser Thr His His Asn Val Arg Leu Leu Met Leu Asp  
290 295 300

Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val Leu Thr Asp  
305 310 315 320

Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr Leu  
325 330 335

Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg Leu  
340 345 350

Phe Pro Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser Lys  
355 360 365

Phe Trp Glu Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met Gln  
370 375 380

Tyr Ser His Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly Trp  
385 390 395 400

Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp Val  
405 410 415

Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr Lys Asp Thr  
420 425 430

Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys Phe  
435 440 445

Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys Asn  
450 455 460

Asp Leu Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val Val  
465 470 475 480

Val Val Leu Asn Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys Asp  
485 490 495

Pro Ala Val Gly Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile His  
500 505 510

Thr Tyr Leu Trp His Arg Gln Asp Leu Leu Val Asp Thr Met  
515 520 525